## **CLAIMS**

- 1. Nucleotides encoding the full length or part of the nucleocapsid (NP) protein of Newcastle disease virus (NDV).
- 2. The nucleotides as claimed in claim 1 characterised in that it has the following nucleotide sequence:

	10 ATGTCTTCCG	20 TATTCGATGA		40 CTCCTCGCTG	50 CTCAGACTCG	60 CCCCAATGGA
	70 GCTCACGGAG	80 GGGGAGAGAG	90 AGGGAGCACT	100 TTAAGAGTTG	110 AGGTCCCAGT	120 ATTCACTCTT
10	130 AACAGTGACG	140 ATCCAGAAGA	150 TAGATGGAAT	160 TTTGCGGTAT	170 TCTGTCTTCG	180 GATTGCTGTT
	190 AGCGAGGACG	200 CCAACAAACC	210 GCTCAGGCAA	220 GGTGCTCTCA	230 TATCCCTCCT	240 GTGCTCCCAT
15	250 TCTCAAGTGA	260 TGAGGAACCA	270 TGTTGCCCTT	280 GCAGGAAAAC	290 AGAATGAGGC	300 TACACTGACT
	310 GTTCTTGAGA	320 TCGATGGTTT	330 TACCAGCAGC	340 GTGCCTCAGT	350 TCAACAACAG	360 GAGTGGGGTG
	370 TCTGAGGAGA	380 GAGCACAGAG	390 ATTCATGGTG	400 ATAGCAGGGT	410 CTCTCCCTCG	420 GGCGTGCAGT
20	430 AACGGTACTC		450 GGCTGGGGTT	460 GAAGATGATG	470 CACCAGAAGA	
	490 ACTCTGGAAA			520 CAGGTATGGG		
25	550 ACTGCATATG			580 ACAAGAAGAA		
	610 GGCAGAGTCC			640 CCTGTATGCA		
	670 ATCAGACATT	680 CTCTGGCAGT		700 TTAGTTAGCG		
30	730 ACGGCAGGTG					780 ATACATCAGG
	790 AACACCGGAC					840 CAAGACATCA

	850 GCCCTAGCAC	860 TCAGCAGCCT		880 ATCCAAAAGA	890 TGAAGCAGCT	900 CATGCGTTTA
	910 TATCGGATGA	920 AGGGAGAAAA	930 TGCGCCGTAC	940 ATGACATTGC	950 TAGGTGACAG	960 TGATCAGATG
5	970 AGCTTTGCAC	980 CGGCTGAGTA	990 TGCACAGCTT	1000 TATTCTTTTG	1010 CCATGGGCAT	1020 GGCATCAGTC
	1030 TTAGATAAAG	1040 GAACTGGCAA	1050 ATACCAATTC	1060 GCCAGAGACT	1070 TCATGAGCAC	1080 ATCATTCTGG
10	1090 AGACTCGGGG	1100 TGGAGTATGC	1110 TCAGGCTCAG	1120 GGGAGTAGCA	1130 TCAACGAAGA	1140 CATGGCTGCT
	1150 GAGCTAAAAC	1160 TAACCCCGGC	1170 AGCAAGAAGG		1190 CTGCTGCCCA	1200 ACGAGTGTCT
	1210 GAGGAAACTG	1220 GCAGCGTGGA	1230 TATTCCTACT		1250 GGGTCCTCAC	
15	1270 GATGGAGGCC	1280 CCCGAGCCTC			1310 CGCAAGGGCA	1320 ACCAGATGCC
	1330 GGAGATGGGG	1340 AGACCCAATT	1350 CTTGGATTTG		1370 TGGCGAACAG	1380 CATGCGAGAA
20	1390 GCGCCAAACT	1400 CCGCACAGAG		1420 CCGGAACCCC	1430 CCCCGACTCC	
	1450 CAAGATAACG	1460 ACACCGACTG		1480	1490	1500

- 3. Nucleotides encoding the full length or part of the phosphoprotein (P) of Newcastle disease virus (NDV).
- 4. The nucleotides as claimed in claim 3 characterised in that it has the following nucleotide sequence:

	10	20	30	40	50	60
	ATGGCCACCT	TTACAGATGC	GGAGATAGAT	GATATATTTG	AGACCAGTGG	AACTGTCATT
30	70	80	90	100	110	120
	GACAGCATAA	TTACGGCCCA	GGGTAAATCA	GCAGAGACTG	TCGGAAGGAG	CGCAATCCCA
	130	140	150	160	170	180
	CAAGGCAAGA	CCAAAGCGCT	GAGCATAGCA	TGGGAGAAGC	ATGGGAGCAT	CCAACCATCC
	190	200	210	220	230	240
	ACCAGCCAGG	ACAACCCCGA	CCAACAGGAT	AGACCAGACA	AACAGCTATC	CACACCTGAG
35	250	260	270	280	290	300
	CAGGCGACCC	CACACAACAG	CTCGCCAGCC	ACATCCGCCG	AACCGCTCCC	CACTCAGGCC

	310 GCAGGTGAGG	320 CCGGCGACAC			350 GCAACTCTCT	
	370 CTCGACAAGC	380 TGAGCAATAA	390 ACCATCTAAT	400 GCTAAAAAGG	410 GCCCATGGTC	420 GAGTCCCCAG
5	430 GAAGGATATC	440 ATCAACCTCC	450 GACCCAACAA	460 CATGGGGATC	470 AGCCGAACCG	480 CGGAAACAGC
	490 CAGGAGAGGC	500 TGCGGCACCA	510 AGCCAAGGCC	520 GCCCTGGAA		540 AGACGCGAGC
10	550 ACAGCATATC	560 ATGGACAATG	570 GAAGGAGTCA			600 CCCTCATGTG
	610 CTCCAATCAG	620 GGCAGAGCCA	630 AGACAGTACT	640 CCTGTACCTG		
	670 GTCGACTTTG	680 TGCAGGCGAT	690 GATGACTATG	700 ATGGAGGCGT	710 TATCACAGAA	720 GGTAAGTAAA
15	730 GTCGACTATC	740 AGCTAGACCT	750 AGTCTTAAAG			780 GATGCGGTCT
	790 GAAATCCAAC	800 AGCTAAAAAC	810 ATCTGTTGCG			
20	850 ATTCTGGACC	860 CTGGTTGTGC	870 TAACATTTCA			
	910 TCCCACCCAG	920 TTTTAATTTC	930 AGGCCCCGGA	940 GATCCGTCCC	950 CCTACGTGAC	
	970 GAGATGACAC	980 TCAATAAACT	990 CTCACAACCA	1000 GTACAACACC	1010 CTTCCGAGTT	1020 AATTAAATCT
25	1030 GCCACAGCGG	1040 GCGGACCTGA	1050 TATGGGAGTG	1060 GAAAAGGACA		
	1090 TCGCGCCCGA	1100 TGCATCCAAG				1140 TGCAGCCGGG
30	1150 TCGATTGAAG	1160 AGATCAGAAA				

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5. The NP protein coded according to claim 1 or claim 2 characterised in that it has the following amino acid sequence:

16 L Μ S S V F D E E ATG TCT TCC GTA TTC GAT GAA TAC GAG CAG CTC CTC GCT GCT CAG ACT 35 10 20 32 G E R G S  $\mathbf{T}$ G A H G G N CGC CCC AAT GGA GCT CAC GGA GGG GGA GAG AGA GGG AGC ACT TTA AGA 60 70 80

	33	V E V P V F T L N S D D P E D R 48 GTT GAG GTC CCA GTA TTC ACT CTT AAC AGT GAC GAT CCA GAA GAT AGA 100 110 120 130 140
5	49	W N F A V F C L R I A V S E D A TGG AAT TTT GCG GTA TTC TGT CTT CGG ATT GCT GTT AGC GAG GAC GCC 150 160 170 180 190
	65	N K P L R Q G A L I S L L C S H 80 AAC AAA CCG CTC AGG CAA GGT GCT CTC ATA TCC CTC CTG TGC TCC CAT 200 210 220 230 240
10	81	S Q V M R N H V A L A G K Q N E 96 TCT CAA GTG ATG AGG AAC CAT GTT GCC CTT GCA GGA AAA CAG AAT GAG 250 260 270 280
15	97	A T L T V L E I D G F T S S V P 112 GCT ACA CTG ACT GTT CTT GAG ATC GAT GGT TTT ACC AGC AGC GTG CCT 290 300 310 320 330
	113	Q F N N R S G V S E E R A Q R F 128 CAG TTC AAC AAC AGG AGT GGG GTG TCT GAG GAG AGA GCA CAG AGA TTC 340 350 360 370 380
20	129	M V I A G S L P R A C S N G T P 144 ATG GTG ATA GCA GGG TCT CTC CCT CGG GCG TGC AGT AAC GGT ACT CCG 390 400 410 420 430
	145	F V T A G V E D D A P E D I T D 160 TTC GTC ACG GCT GGG GTT GAA GAT GCA CCA GAA GAT ATC ACT GAT 440 450 460 470 480
25	161	T L E R I L S I Q A Q V W V T V 176 ACT CTG GAA AGA ATC CTG TCT ATC CAG GCT CAG GTA TGG GTC ACA GTA 490 500 510 520
30	177	A K A M T A Y E T A D E S E T R 192 GCG AAG GCC ATG ACT GCA TAT GAG ACA GCA GAT GAG TCG GAA ACA AGA 530 540 550 560 570
	193	R I N K Y M Q Q G R V Q K K Y I 208 AGA ATC AAT AAG TAC ATG CAG CAA GGC AGA GTC CAG AAG AAG TAC ATC 580 590 600 610 620
35	209	L H P V C R S A I Q L T I R H S 224 CTC CAC CCT GTA TGC AGG AGT GCA ATT CAA CTC ACA ATC AGA CAT TCT 630 640 650 660 670
	225	L A V R I F L V S E L K R G R N 240 CTG GCA GTC CGC ATT TTC TTA GTT AGC GAG CTT AAG AGA GGC CGC AAT 680 690 700 710 720
40	241	T A G G S S T Y Y N L V G D V D 256 ACG GCA GGT GGG AGC TCC ACG TAT TAC AAC TTA GTA GGG GAT GTA GAC 730 740 750 760
45	257	S Y I R N T G L T A F F L T L K 272 TCA TAC ATC AGG AAC ACC GGA CTT ACT GCA TTC TTC CTT ACA CTC AAA 770 780 790 800 810
	273	Y G I N T K T S A L A L S S L T 288 TAT GGA ATT AAT ACC AAG ACA TCA GCC CTA GCA CTC AGC AGC CTC ACA 820 830 840 850 860
50	289	G D I Q K M K Q L M R L Y R M K 304 GGC GAT ATC CAA AAG ATG AAG CAG CTC ATG CGT TTA TAT CGG ATG AAG 870 880 890 900 910

		305	G GGA		N <b>AAT</b> 920	A GCG	P CCG	Y TAC 930	M ATG	T ACA		L CTA 10	G GGT	D GAC	S AGT 950	D GAT	Q CAG	M ATG 960	320
	L CTT 990	Y TAT	S TCT	F TTT 100		M ATG	G GGC	336											
	10	337 1	M ATG 010	A GCA		V GTC 1020	L TTA	D GAT	K AAA 103		T ACT		K AAA 040	Y TAC		F TTC 1050	A GCC	R AGA	352
		353	D GAC 106		M ATG		T ACA 070	S TCA		W TGG 1080	R AGA	L CTC	G GGG 10	V GTG 90	E GAG		A GCT 100	Q CAG	368
	15	369		Q CAG L110	G GGG	S AGT	S AGC 11:		N AAC		D GAC 130	M ATG		A GCT 1140	E GAG	L CTA	K AAA 11	L CTA 50	384
		385	T ACC	CCG	A GCA 160	A GCA		R AGG 1170	G GGC	L CTG	A GCA 11		A GCT	A GCC 1	Q CAA 190	R CGA		S TCT 1200	400
Sitter and the same of the same time.	20	401		E GAA	T ACT 12		S AGC		D GAT 220	I ATT			Q CAA	Q CAA	A GCC 12		V GTC	L CTC	416
- 100 mm - 400 mm - 4	25	417	T ACT 250	G GGG		S AGC 1260	D GAT	G GGA	G GGC 12		R CGA		S TCT 280	Q CAG		G GGA 1290	S TCG	N AAC	432
		433			Q CAA		Q CAA 310	P CCA		A GCC 1320		D GAT	G GGG 13		T ACC		F TTC 340	L TTG	448
100 to 10	30	449	GAT	L TTG 1350	M ATG	R AGA	A GCA 13		A GCG		s AGC 370	M ATG		E GAA 1380		P CCA	N AAC 13	S TCC 90	464
		465	A GCA		S AGC 400	T ACC		H CAC 1410		E GAA	P CCC 14		P CCG		P CCC 430	G GGG		S TCC 1440	480
	35	481	Q CAA	D GAT	N AAC 14			D GAC 1		G GGG		* TGA 1470							490

6. The P protein coded according to claim 3 or claim 4 characterised in that it has the following amino acid sequence:

40	1	M																16	
		ATG	GCC	ACC	TTT	ACA	GAT	GCG	GAG	ATA	GAT	GAT	ATA	TTT	GAG	ACC	AGT		
		1		-	10			20			30			4	40				
	17	G	т	V	I	D	S	I	I	т	A	Q	G	K	s	A	E	32	
		GGA	ACT	GTC	ATT	GAC	AGC	ATA	ATT	ACG	GCC	CAG	GGT	AAA	TCA	GCA	GAG		
45		50			60			-	7.0			80			90				

G R S A I P Q G K T K A L S

1 mag \* # 13 m #I 

	305	L TTA		S TCA 920	G GGC			D GAT		TCC		Y TAC		T ACA 950	Q CAA	G GGG	G GGT 960	320
5	321	E GAG	M ATG	T ACA 97		N AAT		L CTC 980	S TCA	Q CAA	P CCA 990	V GTA	Q CAA	H CAC 100		S TCC	E GAG	336
		TTA				GCC				GGA				GGA			K AAG	352
10	353	D GAC 106		V GTC		A GCA )70		I ATC						H CAT		S AGC 100	S TCC	368
15	369			K AAG	L CTC			K AAG						S TCG	I ATT	E GAA 11		384
	385	I ATC	AGA	k aag 160	I ATC		R CGC 1170	L CTT	A GCA	L CTA 118	N AAT 80	G GGC	* TAA					396

- 7. A recombinant expression plasmid containing the NDV nucleocapsid gene as claimed in claim 1 or claim 2.
- 8. A recombinant expression plasmid containing the NDV phosphoprotein gene as claimed in claim 3 or claim 4.
- 9. The recombinant expression plasmid according to claim 7 which is the expression plasmid pTrcHis2-NP constructed by cloning the NDV nucleocapsid gene of claims 1 or 2 into vector pTrcHis2.
- 10. The recombinant expression plasmid according to claim 8 which is the expression plasmid pTrcHis2-P constructed by cloning the NDV phosphoprotein gene of claims 3 or 4 into vector pTrcHis2.
- 11. A transformed *Escherichia coli* with the recombinant expression plasmid according to claim 7 or claim 9.
- 12. A transformed *Escherichia coli* with the recombinant expression plasmid according to claim 8 or claim 10.

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- 13. The transformed microorganism according to claim 11, which is the transformed *E. coli* TOP10 (pTrcHis2-NP) produced by introducing the recombinant expression plasmid of claim 7 or claim 9 into *E. coli* TOP10.
- 14. The transformed microorganism according to claim 12, which is the transformed *E. coli* (pTrcHis2-P) produced by introducing the recombinant expression plasmid of claim 8 or claim 10 into *E. coli* TOP 10.
- 15. A fused or non-fused form of NDV nucleocapsid protein isolated and purified from culture of the transformed microorganism of claim 11 or claim 13 characterised in that it has the following amino acid sequence:

	10	1	М	S	S	V	F	D	E	Y	E	0	L	L	A	A	0	т	16
	10	_	ATG 1	TCT		GTA LO	TTC					_		CTC	GCT	GCT 10	CĀG	ACT	
7 7	15	17	R CGC 50	CCC	N AAT	G GGA 60	A GCT	H CAC		G GGG 70	G GGA	E GAG	R AGA 80	G GGG	S AGC	T ACT 90	L TTA	R AGA	32
		33		E GAG )0	V GTC	CCA	V GTA L10	F TTC	T ACT	L CTT 120	N AAC	S AGT	D GAC		P CCA		D GAT L40	R AGA	48
The Local Will should have been seen to be suited to the local states of the local sta	20	49	W TGG	N AAT 150	F TTT		V GTA 16			L CTT		I ATT	A GCT	V GTT 180	S AGC	E GAG		A GCC 90	64
*		65	N AAC	AAA	P CCG 200	L CTC	R AGG	Q CAA 210	G GGT	A GCT	L CTC 22		S TCC		L CTG 230	C TGC	S TCC	H CAT 240	80
	25	81	S TCT	Q CAA	V GTG 25		R AGG		H CAT 260	V GTT	A GCC	L CTT 270	A GCA	G GGA	K AAA 28		N AAT	E GAG	96
	30	97	A GCT 290	T ACA	L CTG	T ACT 300	V GTT	L CTT		I ATC LO	D GAT		F TTT 320	T ACC	S AGC	S AGC 330	V GTG	P CCT	112
		113	CÃG	F TTC 40	N AAC		R AGG 350	S AGT		V GTG 360	S TCT	E GAG		R AGA 70	A GCA		R AGA 380	F TTC	128
	35	129	M ATG	V GTG 390	I ATA	A GCA	G GGG 40		L CTC		R CGG 110	A GCG	C TGC	S AGT 420	N AAC	G GGT		P CCG 30	144
		145	F TTC		T ACG 440	A GCT	G GGG	V GTT 450	E GAA	D GAT		A GCA 60	P CCA		D GAT 470	I ATC	T ACT	D GAT 480	160
	40	161	T ACT	L CTG		R AGA 90	I ATC		S TCT 500	I ATC	Q CAG	A GCT 510	Q CAG	V GTA	W TGG 52	V GTC 20	T ACA	V GTA	176

		177	A GCG 530	K AAG	A GCC	M ATG 540	T ACT	A GCA		E GAG 50	T ACA		D GAT 560	E GAG	S TCG	E GAA 570	T ACA	R AGA	192
	5	193		I ATC 30	N AAT		Y TAC 590	M ATG	Q CAG	Q CAA 600	G GGC	R AGA	GTC	Q CAG 10	K AAG		Y TAC 620	I ATC	208
		209	L CTC	H CAC 630	P CCT	V GTA		R AGG 10	S AGT		I ATT 550	Q CAA	L CTC	T ACA 660	I ATC	R AGA		S TCT 70	224
	10	225	L CTG		V GTC 680	R CGC	I ATT	F TTC 690	L TTA	V GTT			L CTT		R AGA 710	G GGC	R CGC	N AAT 720	240
	15	241	T ACG	A GCA	G GGT 73	G GGG 30	S AGC		T ACG 740	Y TAT	Y TAC	N AAC 750	L TTA	V GTA		D GAT 60	V GTA	D GAC	256
9		257	S TCA 770	Y TAC	I ATC	R AGG 780	N AAC	T ACC	G GGA 79		T ACT		F TTC 300	F TTC	L CTT	T ACA 810	L CTC	K AAA	272
	20	273		G GGA 20	I ATT		T ACC 330	K AAG	T ACA	S TCA 840	A GCC	L CTA		L CTC 50	S AGC		L CTC 360	T ACA	288
		289	G GGC	D GAT 870	I ATC		K AAG 88		K AAG		L CTC 390	M ATG		L TTA 900	Y TAT	R CGG		K AAG LO	304
1000 - 3000 - 300 - 3000 - 3000 - 3000 - 3000 - 300 -	25	305	G GGA		N AAT 920	A GCG	P CCG	Y TAC 930	M ATG	T ACA	L TTG 94		G GGT		S AGT 950	D GAT	Q CAG	M ATG 960	320
# 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	30	321	S AGC	F TTT	A GCA 9		A GCT		Y TAT 080	A GCA	Q CAG	L CTT 990	Y TAT	S TCT	F TTT 100		M ATG	G GGC	336
		337 1	M ATG 1010	A GCA	S TCA	V GTC 1020	L TTA	D GAT	K AAA 103			G GGC 10		Y TAC		F TTC 1050	A GCC	R AGA	352
	35	353	D GAC 100		M ATG													Q CAG	368
		369			G GGG		S AGC 112	ATC			GAC		GCT	A GCT 1140		L CTA			384
	40	385		CCG	A GCA 160				G GGC			GCT		GCC					400
	45	401		E GAA	T ACT 12:		AGC	V GTG 12	GAT				Q CAA	Q CAA				L CTC	416
			T ACT 1250	G GGG		S AGC 1260	D GAT		G GGC 12		R CGA	GCC					S TCG	N AAC	432
	50	433			Q CAA	GGG	Q CAA 310	P CCA	GAT	A GCC L320	GGA	D GAT			T ACC	CAA	F TTC 340		448

IN NORTH MENT DE BOTTON EN EN HAND DE MAN DE LE MAN EN MAN DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPAN

	449	D L M R A V A N S M R E A P N S 40 GAT TTG ATG AGA GCA GTG GCG AAC AGC ATG CGA GAA GCG CCA AAC TCC 1350 1360 1370 1380 1390	54
5	465	A Q S T T H P E P P P T P G P S 48 GCA CAG AGC ACC CAC CCG GAA CCC CCC CCG ACT CCC GGG CCA TCC 1400 1410 1420 1430 1440	30
	481	Q D N D T D W G Y * CAA GAT AAC GAC ACC GAC TGG GGG TAT TGA 1450 1460 1470	90
10		16. A fused or non-fused form of NDV phosphoprotein isolated and purified fi	com
		culture of the transformed microorganism of claim 12 or claim	14
		characterised in that it has the following amino acid sequence:	
	1		16
15		ATG GCC ACC TTT ACA GAT GCG GAG ATA GAT GAT ATA TTT GAG ACC AGT 1 10 20 30 40	
	17	G T V I D S I I T A Q G K S A E GGA ACT GTC ATT GAC AGC ATA ATT ACG GCC CAG GGT AAA TCA GCA GAG 50 60 70 80 90	32
20	33	T V G R S A I P Q G K T K A L S ACT GTC GGA AGG AGC GCA ATC CCA CAA GGC AAG ACC AAA GCG CTG AGC 100 110 120 130 140	48
	49	I A W E K H G S I Q P S T S Q D ATA GCA TGG GAG AAG CAT GGG AGC ATC CAA CCA TCC ACC AGC CAG GAC 150 160 170 180 190	64
25	65	N P D Q Q D R P D K Q L S T P E AAC CCC GAC CAA CAG GAT AGA CCA GAC AAA CAG CTA TCC ACA CCT GAG 200 210 220 230 240	80
30	81	Q A T P H N S S P A T S A E P L CAG GCG ACC CCA CAC AAC AGC TCG CCA GCC ACA TCC GCC GAA CCG CTC 250 260 270 280	96
		P T Q A A G E A G D T Q L K T G 1 CCC ACT CAG GCC GCA GGT GAG GCC GGC GAC ACA CAG CTC AAG ACC GGA 290 300 310 320 330	12
35	113	A S N S L L S M L D K L S N K P 1 GCA AGC AAC TCT CTT CTG TCT ATG CTC GAC AAG CTG AGC AAT AAA CCA 340 350 360 370 380	28
	129	S N A K K G P W S S P Q E G Y H 1 TCT AAT GCT AAA AAG GGC CCA TGG TCG AGT CCC CAG GAA GGA TAT CAT 390 400 410 420 430	.44
40	145	Q P P T Q Q H G D Q P N R G N S 1 CAA CCT CCG ACC CAA CAA CAT GGG GAT CAG CCG AAC CGC GGA AAC AGC 440 450 460 470 480	.60
	161	Q E R L R H Q A K A A P G S R G 1 CAG GAG AGG CTG CGG CAC CAA GCC AAG GCC GCC CCT GGA AGC CGG GGC 490 500 510 520	.76

		177	T D ACA GAC 530		S T AGC ACA 540	A GCA	Y H TAT CA 550		Q W CAA TGG 560	K E AAG GAG	s TCA ( 570	Q L CAA CTA	192
	5	193	S A TCA GCI 580	G GGT	A T GCA ACC 590	P CCT	H V CAT GT 60	G CTC		G Q GGG CAG	S GAGC 0		208
		209	S T AGT ACT 630			V GTG 40	D H GAT CA		Q P CAG CCA	P V CCT GTC	D C GAC 1	F V TTT GTG 670	224
	10	225	Q A CAG GCG	M ATG . 680	M T ATG ACT	M ATG 690	M E ATG GA			Q K CAG AAG 710	V G GTA <i>F</i>	S K AGT AAA 720	240
	15	241	V D GTC GAC	Y TAT 73			L V CTA GT	C TTA	K Q AAG CAG 750	T S ACA TCO	S TCC A '60	I P ATC CCT	256
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		257	M M ATG ATG 770		S E TCT GAA 780	I ATC	Q Q CAA CA 790		K T AAA ACA 800	S V	A GCG C 810	V M GTC ATG	272
tions are the two that the first from the first first first first flash	20	273	E A GAA GCT 820	N 'AAT	L G TTA GGC 830	M ATG	M K ATG AA 84	A ATT		P G CCT GG1 50	C TGT (		288
		289	I S ATT TCA 870			D GAT 80	L R CTG CG		V A GTC GCC	R S CGG TCC 900	H C CAC (	P V CCA GTT 910	304
A A A A A A A A A A A A A A A A A A A	25	305	L I TTA ATT	S 'TCA 920	G P GGC CCC	G GGA 930	D P GAT CC			V T GTG ACA 950	Q A CAA (	G G GGG GGT 960	320
*** **********************************	30	321	E M GAG ATG	T ACA 97			L S CTC TC	A CÃA	P V CCA GTA 990	Q H CAA CAC	P C CCT T	S E FCC GAG	336
		337	L I TTA ATT 1010		S A TCT GCC 020	T ACA	A G GCG GG 1030		P D CCT GAT 1040	M G ATG GGA	V A GTG 0 1050	E K Gaa aag	352
	35	353	D T GAC ACT 1060	V GTC	R A CGT GCA 1070	L TTG	I T ATC AC 108	C TCG		M H ATG CAT 90	P CCA #		368
		369	S A TCA GCT 1110	' AAG			AAG CT		GCA GCC	G S GGG TCC 1140		E E GAA GAG 1150	384
	40	385		K AAG .160	I K ATC AAG	R CGC 1170	L A		AAT GGC	* TAA			396